

IN THE CLAIMS:

The claims are pending as follows:

1. (Previously Presented) A primer design system, comprising:
 - means for selecting at least one genomic DNA nucleotide sequence from a database including a plurality of DNA nucleotide sequences;
 - means for predicting a plurality of exons of said selected DNA nucleotide and for storing positions of the predicted exons;
 - means for using each of the predicted exons as a template to design one corresponding primer pair for each of the predicted exons and for designing corresponding primer pairs for the predicted exons simultaneously; and
 - means for automatically collating said plurality of primer pairs with said predicted exons and the DNA nucleotide sequence.
2. (Previously Presented) A primer design system according to claim 1, further comprising means for selecting a plurality of primer pairs meeting certain selection conditions from the designed primer pairs.
3. (Previously Presented) A primer design system according to claim 2, said selection conditions include at least one of a predetermined base length, a range of GC content and a range of T_m.
4. (Previously Presented) A primer design system according to claim 1, further comprising means for evaluating specificity of each designed primer or primer pair.
- 5-29. (Cancelled)
30. (Previously Presented) A method for designing primers, comprising the steps of:
 - selecting at least one DNA nucleotide sequence from a genomic DNA database;
 - predicting a plurality of exons of said selected DNA nucleotide;
 - using each of the predicted exons as a template to design one corresponding primer pair for each of the predicted exons and for designing corresponding primer pairs for the predicted exons simultaneously; and

automatically collating said plurality of primer pairs with said predicted exons and the DNA nucleotide sequence.

31. (Previously Presented) A method for designing primers according to claim 30, further comprising a step of selecting a plurality of primer pairs meeting certain selection conditions from said plurality of designed primer pairs, wherein said extraction conditions include at least one of a predetermined base length, a GC content, T_m .
32. (Previously Presented) A method for designing primers according to claim 30, further comprising a step of evaluating specificity of each designed primer or primer pair.
33. (Previously Presented) A primer design system according to claim 1, further comprising randomly dividing fragments of a genomic DNA as templates for exon prediction.
34. (Previously Presented) A primer design system, comprising:
 - means for selecting at least one genomic DNA nucleotide sequence from a database including a plurality of DNA nucleotide sequences;
 - means for predicting a plurality of exons of said selected DNA nucleotide and for storing positions of the predicted exons;
 - means for using each of the predicted exons as a template to design one corresponding primer pair for each of the predicted exons and for designing corresponding primer pairs for the predicted exons simultaneously; and
 - means for evaluating specificity of each designed primer or each designed primer pair.
35. (Previously Presented) A primer design system according to claim 34, wherein the means for evaluating specificity evaluates each designed primer by conducting homology searches for a full sequence of the primer via at least one repeat database and at least one genome database.
36. (Previously Presented) A primer design system according to claim 34, wherein the means for evaluating specificity evaluates each designed primer by conducting a homology

search for any undesirable sequence contained therein.

37. (Previously Presented) A primer design system according to claim 34, wherein the means for evaluating specificity evaluates each designed primer pair by conducting justification checks on each multiplication region in the DNA which contains an exact sequence as the primer but positioned elsewhere on the DNA.